

Figure 1

Match 70.5%; QryMatch 68.4%; Matches 572; Conservative 105; Mismatches 121;
Indels 13; Gaps 6;

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*****
ZPEP_m      1 MDQREILQQLLKBAQKGCNSEEFASEFLKKGQSTKYKADKIYPTTVAQRPKIKGORY 60
SuPTP04_h   1 MDQREILQKFLDEAQSKITKZEFANEEFLKKGQSTKYKADKIYPTTVAQRPKIKGORY 60

*****
ZPEP_m      61 KDILFYDHSVLVELSLITSDESSSYINASFIKGVYGPWAYIATQGPLSTTLDFWRHWY 120
SuPTP04_h   61 KDILFYDYSRVELSLITSDESSSYIDANFIKGVYGPWAYIATQGPLSTTLDFWRHWY 120

*****
ZPEP_m      121 RILVIVMACMEFEMGKGCERYWAEPOETQLQFGPFSISCEAEKCKSDYKIRTLKAKFN 180
SuPTP04_h   121 SVLIIVMACMEYEMGKGCERYWAEPEMQLSEFGPFSVSCAEKCKSDYIIRTLKAKFN 180

*****
ZPEP_m      181 ETRIIVQPHYKWPFDHVPSSIDPILQLIWMRCYQEDDCVPICIHCSAGCGRTGVICAV 240
SuPTP04_h   181 ETRIIVQPHYKWPFDHVPSSIDPILQLIWMRCYQEDDCVPICIHCSAGCGRTGVICAI 240

*****
ZPEP_m      241 DVTWMLLKDGIIIPKQFSVFNLIQEMTQRPBLVQTQEQVELVYSAVLELFKRMMDVISEN 300
SuPTP04_h   241 DVTWMLLKDGIIIPENFSVFLIREMTQRPBLVQTQEQVELVYSAVLELFKRMMDVIRDK 300

*****
ZPEP_m      301 HLCREIQACCSIEQSLTVEADSCFLDLPKNAMRDVKTINQHSKQGAZESTGGSSSLGLR 360
SuPTP04_h   301 HSCGESQAKHCIPKQNTLQADSYSPNLKSTTKAAQNTNQR---TKMEIKESSEDFR 357

*****
ZPEP_m      361 TSTMNAEEELVLHSAKSSPSFNCLELNCGCNNKAVITRNGQARASPVUGELQKYQSLDF 420
SuPTP04_h   358 TSEISAKEELVLHPAKSSTSDFLELNYSFQKADTTMKWQTKAFFIVGEFLQKHQSLDL 417

*****
ZPEP_m      421 G5MLFGSCPSALPINTADRYHNSKGPVKRTKSTPFELIQQRKTNDLAVGDGFSCLSQLH 480
SuPTP04_h   418 G5LLFEGCSNSKPVNAAGRYFNSKVPITRTKSTPFELIQQRKTNDLAVGDGFSCLSQLH 477

*****
ZPEP_m      481 EHYSLRELQVQRVAMVSSEELNYSLPGAC-----DASCVPRHSPGALRVHLYTSLAEDPY 535
SuPTP04_h   478 DSCFV-ENQAQKVMHVSSAELNYSLPYDSKHQIRNASNVKCHDSSALGVYSYIPLVENPY 536

*****
ZPEP_m      536 FSSSPFNSADSKMSFDLPEKQDGATSPGALLPASSTTSFFYSNPHDSLVMNTLTSFSPPL 595
SuPTP04_h   537 FSSWPPSGTSSKMSLDLPEKQDGVFPSSLLPTSSTSLFSYNSHDSLNLNPTNISSLL 596

*****
ZPEP_m      596 NQETAVEAPSRRTDDEIPPLPERTPESFIVVEEAGEPSFRVTESLP--LVVTFGASPEC 653
SuPTP04_h   597 NQESAVLATAPRIDDEIPPLPVRTPESFIVVEEAGEPSFNVPKSLSSAVKVKIGTSLEW 656

*****
ZPEP_m      654 SGTSE-MKSHDSVGFTPSKGVKLRSPKSDRHQD-GSPPPPLPERTLESFFLADEDCIQAQ 711
SuPTP04_h   657 GGTSEPKGFDDSVILRPSKSVKLRSPKSELHQDRSSPPPPPLPERTLESFFLADEDCIQAQ 716

*****
ZPEP_m      712 AVQTSSTSYPTTENSTSSKQTLRTPGKSFTTRSKSLKIFRANKSVNCS SSPKPTERVQ 771
SuPTP04_h   717 SIETYSTSYPTMENSTSSKQTLKTPGKSFTTRSKSLKILRANKGICNSCPFNKPAZSVQ 776

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ZPEP_m      772 PKVSSSFLNFGFGNRF5KPKGPRNPPSAWAM 802
SuPTP04_h   777 SNVSSSFLNFGFANRF5KPKGPRNPPPTANI 807
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